

Pt/10

**CRF Errors Edited by the STIC Systems  
Branch**

Serial Number: 10/509,422

CRF Edit Date: 10/6/04  
Edited by: Na

**ENTERED**  
Realigned nucleic acid amino acid numbers/text in cases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

3,4

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Deleted: \_\_\_ invalid beginning/end-of-file text ; \_\_\_ page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:



PCT

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION:** US/10/509,422

**DATE:** 10/06/2004  
**TIME:** 16:26:11

**Input Set :** A:\pto.amc.TXT  
**Output Set:** N:\CRF4\10062004\J509422.raw

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6 <110> APPLICANT: Liou, Simon
8 <120> TITLE OF INVENTION: Human BMP2 Inducible Kinases
10 <130> FILE REFERENCE: 004974.01015
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/509,422
C--> 12 <141> CURRENT FILING DATE: 2004-09-24
12 <150> PRIOR APPLICATION NUMBER: PCT/EP03/080825
13 <151> PRIOR FILING DATE: 2003-03-20
15 <150> PRIOR APPLICATION NUMBER: US 60/367,512
16 <151> PRIOR FILING DATE: 2002-03-27
18 <150> PRIOR APPLICATION NUMBER: US 60/406,936
19 <151> PRIOR FILING DATE: 2002-08-30
21 <160> NUMBER OF SEQ ID NOS: 9
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 3507
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
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32 ggccgggctg gcggggccgg gcccggggcc ggctgcggct cccggggctc gtccgtgggg 120
33 gtccgggtgt tcgcggtcgg ccgcaccag gtcaccctgg aagagtcgtt ggccgaagg 180
34 ggattctcca cagtttcct cgtgcgtact cacggtgaa tccgatgtgc attgaagcga 240
35 atgtatgtca ataacatgcc agacctaattt gtttgaaaa gggaaattac aattatgaaa 300
36 gagctatctg gtcacaaaaa tattgtggc tattttggact gtgtgttta ttcaatttagt 360
37 gataatgtat gggaaatctt tatcttaatgtt gaatattgtc gagctggaca ggttgtaat 420
38 caaatgaata agaagctaca gacgggtttt acagaaccag aagtgttaca gatattctgt 480
39 gatacctgtg aagctgtgc aaggttgcattt cagtgttgc ctccaaataat tcaccggat 540
40 ctgaaggtag aaaatattttt gtgaatgtt ggtggaaact atgtacttt tgactttggc 600
41 agtgcacta ataaatttct taatcctcaa aaagatggag ttaatgttagt agaagaagaa 660
42 attaaaaagt atacaactct gtcatacaga gcccctgaaa tgatcaacct ttatggaggg 720
43 aaacccatca ccaccaaggc tgatatctgg gcactggat gtctactcta taaactttgt 780
44 ttcttcactc ttccctttgg tgagagtca gttgttatct gtgtatggcaa cttcaccatc 840
45 ccagacaatt ctcgttactc ccgtaacata cattgtttaa taaggttcat gcttgaacca 900
46 gatccggAAC atagacctga tatatttcaa gtgtcatatt ttgcattttaa atttgcggaa 960
47 aaggattgtc cagtctccaa catcaataat tcttcttattc cttcagctct tcctgaaccg 1020
48 atgactgcta gtgaaggcgc tgtagggaaa agccaaataa aagccagaat aacagatacc 1080
49 attggaccaa cagaaacctc aattgcacca agacaaagac caaaggccaa ctctgtact 1140
50 actgcactc ccagtgtgc gaccattcaa agttcagcaa cacctgtttaa agtccttgct 1200
51 cctggtaat tcggtaacca tagacccaaa ggggcactaa gacctggaaa tggccctgaa 1260
52 attttattgg gtcaggacc tcctcagcagc cccgcacagc agcatagagt actccagcaa 1320
53 ctacagcagg gagattggag attacagcaa ctccattac agcatcgta tcctcaccag 1380
54 cagcagcagc agcagcagca gcaacagcaa cagcagcagc agcaacagaca acagcagcag 1440
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56 atgcagcagt	atcaacatgc	aacacagcag	caacagatgc	ttcaacaaca	attttaatg	1560
57 cattcggtat	atcaaccaca	accttctgca	tcacagtatc	ctacaatgat	gccgcagtat	1620
58 cagcaggctt	tctttcaaca	gcagatgcta	gctcaacatc	agccgtctca	acaacaggca	1680
59 tcacactgaat	atcttacctc	ccctcaagag	ttctcaccag	ccttagtttc	ctacacttca	1740
60 tcacttccag	ctcaggttgg	aaccataatg	gactccctt	atagtgc当地	taggaagta	1800
61 ttttccagt	cagttgctga	taaagaggcc	attgcaaatt	tcacaaatca	gaagaacatc	1860
62 agcaatccac	ctgataatgtc	agggtggaa	cctttggag	aggataattt	ctctaagtt	1920
63 acagaagagg	aactattgga	cagagaattt	gaccttctaa	gatcaaata	gctcgaggag	1980
64 agagcatct	cagataagaa	tgttagactca	cttctgctc	cacataacca	tcctccagaa	2040
65 gatccttttg	gttctgttcc	tttcatatct	cattcaggca	agggttctcc	tgaaaagaaa	2100
66 gctgaacatt	catctataaa	tcaagaaaaat	ggcactgcaa	accctatcaa	gaacggtaaa	2160
67 acaagtccag	catctaaaga	tcagcggact	ggaaagaaaa	cctcagta	gggtcaagt	2220
68 caaaaaggaa	atgatgaatc	tgaaagtgtat	tttgaatcag	atcccccttc	tcctaaagagc	2280
69 agtgaagagg	aagagcaaga	tgatgaagaa	gttcttcagg	gggaacaagg	agattttat	2340
70 gatgatgata	ctgaaccaga	aaatctgggt	cataggcctc	tcctcatgga	ttctgaagat	2400
71 gagentaag	aggagaaaca	tagctctgat	tctgattatg	agcaggctaa	agcaaagtac	2460
72 agtacatga	gctctgtcta	cagagacaga	tctggcagtg	gaccaaccca	agatcttaat	2520
73 acaataactcc	tcacccctc	ccaattatcc	tctgatgtt	cagtggagac	tcccaaacag	2580
74 gagtttgatg	tatttggcgc	tgcccccttc	tttgcagtgc	gtgctcaaca	gccccagcaa	2640
75 gaaaagaatg	aaaagaacct	ccctcaacac	aggttccctg	ctgcaggact	ggagcaggag	2700
76 gaatttgatg	tattcacaaa	ggcgcctttt	agcaagaagg	tgaatgtaca	agaatgccat	2760
77 gcagtggggc	ctgaggcaca	tactatccc	gttatccc	aaagtgtaga	tgtatttggc	2820
78 tccactccat	ttcagccctt	cctcacatca	acaagaaaa	gtgaaagcaa	tgaggacctt	2880
79 tttgggcttg	tgccctttga	tgaaataacg	gggagccagc	agcaaaaaat	caaacagcgc	2940
80 agcttacaga	aactgttctc	tcgccaaagg	cgcacaaagg	aggatatgtc	caaaagtaat	3000
81 gggaaagcggc	atcatggcac	gccaacttagc	acaaagaaga	cttgaagcc	tacctatcgc	3060
82 actccagaga	gggctcgag	gcacaaaaaa	gtggccgccc	gagactctca	aagtagcaat	3120
83 gaatttttaa	ccatctcaga	ctccaaggag	aacattagtg	ttgcactgac	tatggaaaa	3180
84 gataggggaa	atgtcttaca	acctgaggag	agcctgttgg	acccttcgg	tgccaagccc	3240
85 ttccattctc	cagacctgtc	atggcaccc	ccacatcagg	gcctgagcga	catccgtct	3300
86 gatcacaata	ctgtctgccc	agggcggcca	agacaaaatt	cactacatgg	gtcattccat	3360
87 agtgcagatg	tattgaaaat	ggatgattt	gtgcgtgc	ccttacaga	acttgtgg	3420
88 caaaagcatca	ctccacatca	gtcccaacag	tcccaaccag	tcgaattaga	cccatttgg	3480
89 gctgctccat	ttccttctaa	acagtag				3507

91 <210> SEQ ID NO: 2

92 <211> LENGTH: 1168

93 <212> TYPE: PRT

94 <213> ORGANISM: Homo sapiens

96 <400> SEQUENCE: 2

97 Met Lys Lys Phe Ser Arg Met Pro Lys Ser Glu Gly Gly Ser Gly Gly

98 1	5	10	15
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99 Gly Ala Ala Gly Gly Ala Gly Gly Ala Gly Ala Gly Cys

100 20	25	30
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101 Gly Ser Gly Gly Ser Ser Val Gly Val Arg Val Phe Ala Val Gly Arg

102 35	40	45
--------	----	----

103 His Gln Val Thr Leu Glu Glu Ser Leu Ala Glu Gly Gly Phe Ser Thr

104 50	55	60
--------	----	----

105 Val Phe Leu Val Arg Thr His Gly Gly Ile Arg Cys Ala Leu Lys Arg

106 65	70	75	80
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107 Met Tyr Val Asn Asn Met Pro Asp Leu Asn Val Cys Lys Arg Glu Ile  
 108 85 90 95  
 109 Thr Ile Met Lys Glu Leu Ser Gly His Lys Asn Ile Val Gly Tyr Leu  
 110 100 105 110  
 111 Asp Cys Ala Val Asn Ser Ile Ser Asp Asn Val Trp Glu Val Leu Ile  
 112 115 120 125  
 113 Leu Met Glu Tyr Cys Arg Ala Gly Gln Val Val Asn Gln Met Asn Lys  
 114 130 135 140  
 115 Lys Leu Gln Thr Gly Phe Thr Glu Pro Glu Val Leu Gln Ile Phe Cys  
 116 145 150 155 160  
 117 Asp Thr Cys Glu Ala Val Ala Arg Leu His Gln Cys Lys Thr Pro Ile  
 118 165 170 175  
 119 Ile His Arg Asp Leu Lys Val Glu Asn Ile Leu Leu Asn Asp Gly Gly  
 120 180 185 190  
 121 Asn Tyr Val Leu Cys Asp Phe Gly Ser Ala Thr Asn Lys Phe Leu Asn  
 122 195 200 205  
 123 Pro Gln Lys Asp Gly Val Asn Val Val Glu Glu Glu Ile Lys Lys Tyr  
 124 210 215 220  
 125 Thr Thr Leu Ser Tyr Arg Ala Pro Glu Met Ile Asn Leu Tyr Gly Gly  
 126 225 230 235 240  
 127 Lys Pro Ile Thr Thr Lys Ala Asp Ile Trp Ala Leu Gly Cys Leu Leu  
 128 245 250 255  
 129 Tyr Lys Leu Cys Phe Phe Thr Leu Pro Phe Gly Glu Ser Gln Val Ala  
 130 260 265 270  
 131 Ile Cys Asp Gly Asn Phe Thr Ile Pro Asp Asn Ser Arg Tyr Ser Arg  
 132 275 280 285  
 133 Asn Ile His Cys Leu Ile Arg Phe Met Leu Glu Pro Asp Pro Glu His  
 134 290 295 300  
 135 Arg Pro Asp Ile Phe Gln Val Ser Tyr Phe Ala Phe Lys Phe Ala Lys  
 136 305 310 315 320  
 137 Lys Asp Cys Pro Val Ser Asn Ile Asn Asn Ser Ser Ile Pro Ser Ala  
 138 325 330 335  
 139 Leu Pro Glu Pro Met Thr Ala Ser Glu Ala Ala Ala Arg Lys Ser Gln  
 140 340 345 350  
 141 Ile Lys Ala Arg Ile Thr Asp Thr Ile Gly Pro Thr Glu Thr Ser Ile  
 142 355 360 365  
 143 Ala Pro Arg Gln Arg Pro Lys Ala Asn Ser Ala Thr Thr Ala Thr Pro  
 144 370 375 380  
 145 Ser Val Leu Thr Ile Gln Ser Ser Ala Thr Pro Val Lys Val Leu Ala  
 146 385 390 395 400  
 147 Pro Gly Glu Phe Gly Asn His Arg Pro Lys Gly Ala Leu Arg Pro Gly  
 148 405 410 415  
 149 Asn Gly Pro Glu Ile Leu Leu Gly Gln Gly Pro Pro Gln Gln Pro Pro  
 150 420 425 430  
 151 Gln Gln His Arg Val Leu Gln Gln Leu Gln Gln Gly Asp Trp Arg Leu  
 152 435 440 445  
 153 Gln Gln Leu His Leu Gln His Arg His Pro His Gln Gln Gln Gln Gln  
 154 450 455 460  
 155 Gln Gln

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156	465	470	475	480
157	Gln Gln Gln Gln Gln Gln His His His His His His His His Leu Leu			
158		485	490	495
159	Gln Asp Ala Tyr Met Gln Gln Tyr Gln His Ala Thr Gln Gln Gln			
160		500	505	510
161	Met Leu Gln Gln Gln Phe Leu Met His Ser Val Tyr Gln Pro Gln Pro			
162		515	520	525
163	Ser Ala Ser Gln Tyr Pro Thr Met Met Pro Gln Tyr Gln Gln Ala Phe			
164		530	535	540
165	Phe Gln Gln Gln Met Leu Ala Gln His Gln Pro Ser Gln Gln Gln Ala			
166		545	550	555
167				560
168	Ser Pro Glu Tyr Leu Thr Ser Pro Gln Glu Phe Ser Pro Ala Leu Val			
169		565	570	575
170	Ser Tyr Thr Ser Ser Leu Pro Ala Gln Val Gly Thr Ile Met Asp Ser			
171		580	585	590
172	Ser Tyr Ser Ala Asn Arg Gln Val Phe Phe Gln Ser Val Ala Asp Lys			
173		595	600	605
174	Glu Ala Ile Ala Asn Phe Thr Asn Gln Lys Asn Ile Ser Asn Pro Pro			
175		610	615	620
176	Asp Met Ser Gly Trp Asn Pro Phe Gly Glu Asp Asn Phe Ser Lys Leu			
177		625	630	635
178				640
179	Thr Glu Glu Glu Leu Leu Asp Arg Glu Phe Asp Leu Leu Arg Ser Asn			
180		645	650	655
181	Arg Leu Glu Glu Arg Ala Ser Ser Asp Lys Asn Val Asp Ser Leu Ser			
182		660	665	670
183	Ala Pro His Asn His Pro Pro Glu Asp Pro Phe Gly Ser Val Pro Phe			
184		675	680	685
185	Ile Ser His Ser Gly Lys Gly Ser Pro Glu Lys Lys Ala Glu His Ser			
186		690	695	700
187	188	695	700	705
189	Ser Ile Asn Gln Glu Asn Gly Thr Ala Asn Pro Ile Lys Asn Gly Lys			
190		705	710	715
191				720
192	Thr Ser Pro Ala Ser Lys Asp Gln Arg Thr Gly Lys Lys Thr Ser Val			
193		725	730	735
194	Gln Gly Gln Val Gln Lys Gly Asn Asp Glu Ser Glu Ser Asp Phe Glu			
195		740	745	750
196	Ser Asp Pro Pro Ser Pro Lys Ser Ser Glu Glu Glu Gln Asp Asp			
197		755	760	765
198	Glu Glu Val Leu Gln Gly Glu Gln Gly Asp Phe Asn Asp Asp Asp Thr			
199		770	775	780
200	Glu Pro Glu Asn Leu Gly His Arg Pro Leu Leu Met Asp Ser Glu Asp			
201		785	790	795
202				800
203	Glu Glu Glu Glu Lys His Ser Ser Asp Ser Asp Tyr Glu Gln Ala			
204		805	810	815
205	Lys Ala Lys Tyr Ser Asp Met Ser Ser Val Tyr Arg Asp Arg Ser Gly			
206		820	825	830
207	Ser Gly Pro Thr Gln Asp Leu Asn Thr Ile Leu Leu Thr Ser Ala Gln			
208		835	840	845
209	Leu Ser Ser Asp Val Ala Val Glu Thr Pro Lys Gln Glu Phe Asp Val			
210		850	855	860

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205	Phe	Gly	Ala	Val	Pro	Phe	Phe	Ala	Val	Arg	Ala	Gln	Gln	Pro	Gln	Gln
206	865					870				875						880
207	Glu	Lys	Asn	Glu	Lys	Asn	Leu	Pro	Gln	His	Arg	Phe	Pro	Ala	Ala	Gly
208						885				890						895
209	Leu	Glu	Gln	Glu	Glu	Phe	Asp	Val	Phe	Thr	Lys	Ala	Pro	Phe	Ser	Lys
210						900				905						910
211	Lys	Val	Asn	Val	Gln	Glu	Cys	His	Ala	Val	Gly	Pro	Glu	Ala	His	Thr
212						915				920						925
213	Ile	Pro	Gly	Tyr	Pro	Lys	Ser	Val	Asp	Val	Phe	Gly	Ser	Thr	Pro	Phe
214						930				935						940
215	Gln	Pro	Phe	Leu	Thr	Ser	Thr	Ser	Lys	Ser	Glu	Ser	Asn	Glu	Asp	Leu
216						945				950						960
217	Phe	Gly	Leu	Val	Pro	Phe	Asp	Glu	Ile	Thr	Gly	Ser	Gln	Gln	Gln	Lys
218						965				970						975
219	Val	Lys	Gln	Arg	Ser	Leu	Gln	Lys	Leu	Ser	Ser	Arg	Gln	Arg	Arg	Thr
220						980				985						990
221	Lys	Gln	Asp	Met	Ser	Lys	Ser	Asn	Gly	Lys	Arg	His	His	Gly	Thr	Pro
222						995				1000						1005
223	Thr	Ser	Thr	Lys	Lys	Thr	Leu	Lys	Pro	Thr	Tyr	Arg	Thr	Pro	Glu	Arg
224						1010				1015						1020
225	Ala	Arg	Arg	His	Lys	Lys	Val	Gly	Arg	Arg	Asp	Ser	Gln	Ser	Ser	Asn
226						1025				1030						1040
227	Glu	Phe	Leu	Thr	Ile	Ser	Asp	Ser	Lys	Glu	Asn	Ile	Ser	Val	Ala	Leu
228						1045				1050						1055
229	Thr	Asp	Gly	Lys	Asp	Arg	Gly	Asn	Val	Leu	Gln	Pro	Glu	Glu	Ser	Leu
230						1060				1065						1070
231	Leu	Asp	Pro	Phe	Gly	Ala	Lys	Pro	Phe	His	Ser	Pro	Asp	Leu	Ser	Trp
232						1075				1080						1085
233	His	Pro	Pro	His	Gln	Gly	Leu	Ser	Asp	Ile	Arg	Ala	Asp	His	Asn	Thr
234						1090				1095						1100
235	Val	Leu	Pro	Gly	Arg	Pro	Arg	Gln	Asn	Ser	Leu	His	Gly	Ser	Phe	His
236						1105				1110						1120
237	Ser	Ala	Asp	Val	Leu	Lys	Met	Asp	Asp	Phe	Gly	Ala	Val	Pro	Phe	Thr
238						1125				1130						1135
239	Glu	Leu	Val	Val	Gln	Ser	Ile	Thr	Pro	His	Gln	Ser	Gln	Ser	Gln	
240						1140				1145						1150
241	Pro	Val	Glu	Leu	Asp	Pro	Phe	Gly	Ala	Ala	Pro	Phe	Pro	Ser	Lys	Gln
242						1155				1160						1165
245	<210>	SEQ ID NO:	3													
246	<211>	LENGTH:	3704													
247	<212>	TYPE:	DNA													
248	<213>	ORGANISM:	Homo sapiens													
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252	cttgcacgct	ccctgcgccc	tccagctcg	cgccggggacc	atgaagaagt	tctctcgat										120
253	gccccaaatcg	gaggggcgca	gcggccggcg	agcggccgggt	ggcggggctg	gcggggccgg										180
254	ggccggggcc	ggctcgccgt	ccggccggctc	gtccgtgggg	gtccgggtgt	tcgcggtcgg										240
255	ccgcccaccag	gtcacccctgg	aagagtcgt	ggccgaaggt	ggattctcca	cagttttct										300
256	cgtgcgtact	cacgggtggaa	tccgatgtgc	attgaagcga	atgtatgtca	ataacatgcc										360

**VERIFICATION SUMMARY**

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DATE: 10/06/2004

TIME: 16:26:12

Input Set : A:\pto.amc.TXT

Output Set: N:\CRF4\10062004\J509422.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date